Amendments to the Claims:

Please amend the claims as follows. A clean set of all claims are also provided on page 26-31 of Appendix A.

1 through 5. (Cancelled)

6. (Previously presented) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation providing means for improving functionality of the variant cellobiohydrolase with respect to the wild-type cellobiohydrolase.

7. (Currently amended) The nucleic acid molecule of claim 6 wherein the means for improving is selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

~~(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;~~

(d)~~(e)~~ [a]substitution of cysteine at positions 197 and 370;

(e)~~(f)~~ substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f)~~(g)~~ alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

~~(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and~~

(g)~~(i)~~ any combination of the mutations of (a), (b), (c), (d), (e), (f), ~~(g), (h),~~ wherein the positional reference is within ~~an~~ the amino acid sequence of the wild-type ~~encoding a native~~ cellobiohydrolase [I]of SEQ ID NO: 5.

8. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises the proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof.

9. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises the helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof.

10. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for improving comprises substitution of ~~the~~ glycine at position 99.

11. (Currently amended) A method for mutating a nucleic acid encoding a wild type cellobiohydrolase of SEQ ID NO: 5, the method comprising:

mutating the wild type cellobiohydrolase with a mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

~~(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;~~

(d)~~(e)~~ [a]substitution of cysteine at positions 197 and 370;

(e)~~(f)~~ substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f)~~(g)~~ alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

~~(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and~~

(g)~~(i)~~ any combination of the mutations of (a), (b), (c), (d), (e), (f), ~~(g),~~ ~~(h),~~ wherein the positional reference is within ~~an~~ the amino acid sequence of the wild-type ~~encoding a native~~ cellobiohydrolase [I]of SEQ ID NO: 5.

12. (Currently amended) The method of claim 11, wherein the mutation comprises substitution of a ~~the~~ non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

13. (Previously presented) The method of claims 11, wherein the step of mutating comprises site-directed mutagenesis.

14. (Currently amended) The method of claim 11, further comprising a step of shortening a linker region of the wild-type cellobiohydrolase ~~sequence being shortened~~ with respect to wild-type linker region SEQ ID NO: 2 to provide ~~comprises~~ a linker region ~~sequence~~ having a length of from about 6 amino acids ~~20 nucleotides~~ to about 17 amino acids ~~50 nucleotides~~ located, between a catalytic domain and a cellulose binding domain (CBD) of SEQ ID NO: 5.

15. (Currently amended) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 71~~20~~.

16. (Currently amended) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 74~~21~~.

17. (Cancelled).

18. (Cancelled).

19. (Cancelled).

20. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a ~~the~~ cysteine at positions 197 and 370.

21. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a ~~the~~ non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

22. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of an ~~the~~ alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

23. (Cancelled).

24. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises means for enhancing thermostability.

25. (Currently amended) The nucleic acid molecule of claim ~~1~~ 6, wherein the variant cellobiohydrolase comprises a linker region ~~sequence~~ having a length of from about 6 amino acids ~~20 nucleotides~~ to about 17 amino acids ~~50 nucleotides~~ located, between a catalytic domain and a cellulose binding domain (CBD)~~, the linker region sequence being shortened with respect to SEQ ID NO: 2~~.

26. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

~~(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;~~

(d)~~(e)~~ [a]substitution of cysteine at positions 197 and 370;

(e)~~(f)~~ substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f)~~(g)~~ alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

~~(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and~~

(g)~~(i)~~ any combination of the mutations of (a), (b), (c), (d), (e), (f), ~~(g),~~ ~~(h),~~ wherein the positional reference is within ~~an~~ the amino acid sequence of the wild-type ~~encoding a native~~ cellobiohydrolase [I]of SEQ ID NO: 5.

27. (New) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 77.

28. (New) An exoglucanase composition, comprising a combination of exoglucanases selected from the group consisting of exoglucanases defined by claims 15, 16 and 27.

Amendments to the Drawings

Please substitute the attached replacement sheets 1/4 through 4/4 for the corresponding sheets of drawings in the Application to replace Figures 1 through 4 in the Application. Only Figures 1 and 4 have been amended and a mark-up version of these two figures are shown below:

Figure 1. Coding sequence of ~~for~~ the *cbh 1* gene (SEQ ID NO: 4). ~~Small~~ Lower case letters represent the signal sequence, ~~large~~ upper case letters the catalytic domain, bolded italics the linker region, and ~~large~~ upper case underlined the cellulose-binding domain.

atgtatcggaagttggccgtcatctcggccttcttggccacagctcgtgctCAGTCGGCCTGCACTCTCCAATCGGAACTCAC
CCGCCTCTGACATGGCAGAAATGCTCGTCTGGTGGCACGTGCACTCAACAGACAGGCTCCGTG
GTCATCGACGCCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACTGCTACGATGG
CAACACTTGGAGCTCGACCCTATGTCCTGACAACGAGACCTGCGCGAAGAACTGCTGTCTGGA
CGGTGCCGCCTACGCGTCCACGTACGGAGTTACCACGAGCGGTAACAGCCTCTCCATTGGCTT
TGTCACCCAGTCTGCGCAGAAGAACGTTGGCGCTCGCCTTTACCTTATGGCGAGCGACACGAC
CTACCAGGAATTCACCCTGCTTGGCAACGAGTTCTCTTTCGATGTTGATGTTTCGCAGCTGCCG
TGCGGCTTGAACGGAGCTCTCTACTTCGTGTCCATGGACGCGGATGGTGGCGTGAGCAAGTAT
CCCACCAACACCGCTGGCGCCAAGTACGGCACGGGGTACTGTGACAGCCAGTGTCCCCGCGA
TCTGAAGTTCATCAATGGCCAGGCCAACGTTGAGGGCTGGGAGCCGTCATCCAACAACGCGA
ACACGGGCATTGGAGGACACGGAAGCTGCTGCTCTGAGATGGATATCTGGGAGGCCAACTCC
ATCTCCGAGGCTCTTACCCCCCACCCTTGCACGACTGTCGGCCAGGAGATCTGCGAGGGTGAT
GGGTGCGGCGGAACTTACTCCGATAACAGATATGGCGGCACTTGCGATCCCGATGGCTGCGA
CTGGAACCCATACCGCCTGGGCAACACCAGCTTCTACGGCCCTGGCTCAAGCTTTACCCTCGA
TACCACCAAGAAATTGACCGTTGTCACCCAGTTCGAGACGTCGGGTGCCATCAACCGATACTA
TGTCCAGAATGGCGTCACTTTCCAGCAGCCCAACGCCGAGCTTGGTAGTTACTCTGGCAACGA
GCTCAACGATGATTACTGCACAGCTGAGGAGGCAGAATTCGGCGGATCCTCTTTCTCAGACAA
GGGCGGCCTGACTCAGTTCAAGAAGGCTACCTCTGGCGGCATGGTTCTGGTCATGAGTCTGTG
GGATGATTACTACGCCAACATGCTGTGGCTGGACTCCACCTACCCGACAAACGAGACCTCCTC
CACACCCGGTGCCGTGCGCGGAAGCTGCTCCACCAGCTCCGGTGTCCCTGCTCAGGTCGAATC
TCAGTCTCCCAACGCCAAGGTCACCTTCTCCAACATCAAGTTCGGACCCATTGGCAGCACCGG
CAACCCTAGCGGCGGCAAC***CCTCCCGGCGGAAACCCGCCTGGCACCACCACCACCCGCCGCCC***
AGCCACTACCACTGGAAGCTCTCCCGGACCTACCCAGTCTCACTACGGCCAGTGCGGCGGTATT
GGCTACAGCGGCCCCACGGTCTGCGCCAGCGGCACAACTTGCCAGGTCCTGAACCCTTACTAC
TCTCAGTGCCTGTAAAGCTCC

Figure 4. ~~Coding~~ Nucleotide sequence~~,~~ SEQ ID NO: 1~~-19~~, coding for the linker region, SEQ ID NO: 2, of the CBH I protein, ~~*cbh 1* gene, SEQ ID NO: 4,~~ showing additional proline residues ~~nucleotides~~ that effect conformation of the linker region in the protein structure.